AMENDMENTS TO THE CLAIMS

1. **(Currently amended)** A method for identifying and/or quantifying a biological organism ~~or a component thereof~~ in a sample by detecting a nucleotide sequence ~~characteristic~~ of said biological organism, wherein said nucleotide sequence is homologous to at least 4 other nucleotide sequences from other biological organisms, comprising:

amplifying or copying at least one of said homologous nucleotide sequences into target homologous nucleotide sequences using primer pairs which are capable of amplifying or copying at least ~~two~~ four of said target homologous nucleotide sequences from other organisms;

contacting said ~~amplified or copied~~ target homologous nucleotide sequences with single-stranded different capture nucleotide sequences, at least two of said single-stranded capture nucleotide sequences being specific ~~of~~ for at least two of said target homologous nucleotide sequences, said single-stranded capture nucleotide sequences being covalently bound in an array to an insoluble solid support via a spacer which is at least 6.8 nm in length, said array comprising at least four different bound single-stranded capture nucleotide sequences/cm² of solid support surface, and wherein each of said single-stranded capture nucleotide sequences comprises a nucleotide sequence of about 5 to about 60 bases wherein said nucleotide sequence of about 5 to about 60 bases is ~~are~~ able to specifically bind to ~~a~~ one of the target homologous nucleotide sequences without binding to said at least four other homologous nucleotide sequences, wherein said array also contains consensus capture nucleotide sequences for a common detection of said target homologous nucleotide sequences, said consensus capture nucleotide sequences having a length specific of the target comprising between about 10 and about 1000 bases, and~~;~~

detecting specific hybridization of the target homologous nucleotide sequence to said single-stranded capture nucleotide sequences,

wherein said single-stranded capture nucleotide sequence ~~being~~ is bound to the insoluble solid support at a specific location upon the array, and

wherein the binding between said target homologous nucleotide sequence and its corresponding single-stranded capture nucleotide sequence forms a signal at the expected location, the detection of said signal allowing a discrimination of the target homologous

nucleotide sequence being specific of said organism ~~or components of said organism~~ from other organisms ~~or components of said organisms~~ from the same or other groups, sub-groups or sub-sub-groups of said organisms ~~or components of said organisms~~.

2. **(Currently amended)** The method of claim 1, wherein said biological organism ~~or said component of the biological organism~~ is present in the sample among at least 2 other organisms ~~or components of said other organisms~~.

3. **(Currently amended)** The method of claim 1, wherein said biological organism ~~or said component of the biological organism~~ is present in the sample among at least 4 other organisms ~~or components of said other organisms~~.

4. **(Currently amended)** The method of claim 1, further comprising extracting ~~components~~ the nucleotide sequence from said organism.

5. **(Currently amended)** The method of claim 1, further comprising labeling said organism or its ~~components~~ nucleotide sequence as targets.

6. **(Original)** The method of claim 1, wherein said organism is a microorganism.

7. **(Currently amended)** The method of claim 1, further comprising identifying and/or quantifying the presence of several groups, sub-groups or sub-sub-groups of said organisms ~~or components of said organisms~~ being related to each other, wherein the binding between ~~targets~~ target homologous nucleotide sequences and corresponding ~~specific~~ consensus capture ~~molecules~~ nucleotide sequences forms a signal at an expected location allowing the identification of a target nucleotide sequence specific of a group, sub-group or sub-sub-group of organisms ~~comprising said components~~.

8. **(Currently amended)** The method of claim 7, wherein the array contains two categories of capture ~~molecules~~ nucleotide sequences, a first category of capture ~~molecules~~ nucleotide sequences being specific for individual target ~~components~~ nucleotide sequences or their sub-groups and a second category of capture ~~molecules~~ nucleotide sequences being specific for all the ~~components~~ nucleotide sequences of the group.

9. **(Canceled)**

10. **(Canceled)**

11. **(Currently amended)** The method of claim 1 ~~10~~, wherein said ~~second category of~~ consensus capture nucleotide sequences has a sequence ~~length~~ specific ~~of~~ for the target ~~comprised~~ comprising a sequence which is between about 100 and 600 bases in length.

12. **(Currently amended)** The method of claim 1, wherein the amplified target homologous nucleotide sequences are homologous polynucleotides and are discriminated on the array upon corresponding polynucleotide capture sequences.

13. **(Previously presented)** The method of claim 1, wherein the amplified nucleotide sequence is a DNA nucleotide sequence.

14. **(Currently amended)** The method of claim 1, wherein all or most of the amplified nucleotide sequences are obtained by PCR with the same primer pair.

15. **(Currently amended)** The method of claim 1, wherein the presence of any amplified nucleotide sequence is firstly detected during the genetic amplification cycles and thereafter identified on the array.

16. **(Currently amended)** The method of claim 1, wherein the step of detecting the presence of any amplified nucleotide sequences and the genetic amplification step are performed in a same chamber.

17. **(Currently amended)** The method of claim 1, wherein the amplified nucleotide sequence is mRNA first reverse transcribed into cDNA and then amplified with the same primer pair which is capable of amplifying at least two of said homologous mRNA ~~is~~ in said sample.

18. **(Previously presented)** The method of claim 1, wherein the nucleotide sequences are copied by using the same primer pair.

19. **(Canceled)**

20. **(Currently amended)** The method of claim 1 ~~19~~, wherein said spacer is a nucleotide sequence of between about 15 and about 1000 bases.

21. **(Currently amended)** The method of claim 1 ~~19~~, wherein said spacer is a nucleotide sequence of between about 30 and about 120 bases.

22. **(Currently amended)** The method of claim 1 ~~19~~, wherein the spacer is a polymeric chain of at least 10 atoms, selected from the group consisting of poly-ethyleneglycol, polyaminoacids, polyacrylamides, poly-aminosaccharides, polyglucides, polyamides, polyacrylates, polycarbonates, polyepoxides, poly-ester and a mixture thereof.

23. **(Currently amended)** The method of claim 22 ~~19~~, wherein said polymeric chain is branched.

24. **(Canceled)**.

25. **(Currently amended)** The method of claim 1 ~~24~~, wherein the length of the specific sequence of the capture nucleotide sequence able to hybridize with the corresponding target nucleotide sequences is comprised between about 20 and about 30 bases.

26. **(Previously presented)** The method of claim 1, wherein the density of the capture nucleotide sequences bound to the solid support surface at a specific location is greater than 10 fmoles per cm^2 of solid support surface.

27. **(Previously presented)** The method of claim 1, wherein the density of the capture nucleotide sequences bound to the solid support surface at a specific location is greater than 100 fmoles per cm^2 of solid support surface.

28. **(Canceled)**

29. **(Previously presented)** The method of claim 1, wherein the capture nucleotide sequences bound to the solid support surface at a specific location are polynucleotides.

30. **(Previously presented)** The method of claim 1, wherein the target nucleotide sequence(s) to be detected present(s) a homology of greater than about 40% with other homologous nucleotide sequences.

31. **(Previously presented)** The method of claim 1, wherein the target nucleotide sequence(s) to be detected present(s) a homology of greater than about 60% with other homologous nucleotide sequences.

32. **(Previously presented)** The method of claim 1, wherein the target nucleotide sequence(s) to be detected present(s) a homology of greater than about 80% with other homologous nucleotide sequences.

33. **(Previously presented)** The method of claim 1, wherein the target nucleotide sequences are labelled by a marker and wherein the signal resulting from hybridization by complementary bases pairing between the target nucleotide sequence and its corresponding capture nucleotide sequence is obtained from the detection of said marker.

34. **(Previously presented)** The method of claim 1, wherein the target nucleotide sequences are cut into pieces before putting into contact with the single stranded capture nucleotide sequences bound to the solid support.

35. **(Currently amended)** The method of claim 1, wherein other primers are present in the amplification step for the amplification of ~~other nucleotide sequences, such as~~ an antibiotic resistance determining nucleotide sequence.

36. **(Previously presented)** The method of claim 1, wherein the nucleotide sequences to be detected and/or be quantified are RNA sequences submitted to a retro-transcription of the 3' or 5' end by using a member selected from the group consisting of a consensus primer and a stopper sequence.

37. **(Canceled)**

38. **(Currently amended)** The method of claim 1, wherein the solid support comprises single-stranded capture nucleotide sequences specific for the identification of two or more *Staphylococcus* species ~~together with~~ , said solid support further comprises a consensus capture nucleotide ~~consensus~~ sequence for a *Staphylococcus* genus identification.

39. **(Currently amended)** The method of claim 1, wherein the nucleotide sequence to be identified and/or quantified in the sample differs from at least one of its homologous nucleotide sequences present in the sample by one or more base(s).

40. **(Currently amended)** The method of claim 1, wherein the arrays contained two to four single-stranded capture nucleotide sequences differing from each other by one or more base(s).

41. **(Cancelled)**

42. **(Cancelled)**

43. **(Cancelled)**

44. **(Original)** The method of claim 1, wherein the quantification of the organism present in the biological sample is obtained by the quantification of the signal.

45. **(Currently amended)** The method of claim 1, wherein the insoluble solid support is selected from the group consisting of glass, an electronic device, a silicon support, a plastic support, silica, metal and a mixture thereof, wherein said support is prepared ~~in a prepared~~ in a format selected from the group consisting of slides, discs, gel layers and microbeads.

46. **(Previously presented)** The method of claim 6, wherein the microorganism to be identified and/or quantified in the sample belongs to the Staphylococci species selected from the group consisting of *S. aureus, S. epidermidis, S. saprophyticus, S. hominis* and *S. haemolyticus.*

47. **(Previously presented)** The method of claim 6, wherein the microorganism to be identified and/or quantified in the sample belong to the Mycobacteria genus.

48. **(Currently amended)** The method of claim 1, wherein the nucleotide sequence ~~component~~ to be identified and/or quantified in the sample is a sequence which belongs to the MAGE family.

49. **(Currently amended)** The method of claim 1, wherein the nucleotide sequence ~~component~~ to be identified and/or quantified in the sample is a sequence which belongs to the *HLA-A* family.

50. **(Currently amended)** The method of claim 1, wherein the nucleotide sequence ~~component~~ to be identified and/or quantified in the sample is a G protein-coupled receptor.

51. **(Currently amended)** The method of claim 1, wherein the nucleotide sequence ~~component~~ to be identified and/or quantified in the sample is a dopamine receptor.

52. **(Currently amended)** The method of claim 1, wherein the nucleotide sequence ~~component~~ to be identified and/or quantified in the sample is a choline receptor.

53. **(Currently amended)** The method of claim 1, wherein the nucleotide sequence ~~component~~ to be identified and/or quantified in the sample is a histamine receptor.

54. **(Currently amended)** The method of claim 1, wherein the nucleotide sequence ~~component~~ to be identified and/or quantified in the sample is a sequence which belongs the Cytochrome P450 isoforms family.

55. **(Currently amended)** The method of claim 6, wherein the microorganism to be identified and/or quantified in the sample belongs to a Gram-positive or Gram-negative family bacteria.

56. **(Original)** The method of claim 7, wherein the group, sub-group or individual targets correspond to families, genus, species, subtypes or individual organisms.

57. **(Original)** The method of claim 7, wherein the families, genus, species, subtypes or individuals are bacteria.

58. **(Currently amended)** The method of claim 57, wherein bacteria ~~belonging~~ belongs to at least two of the genus families selected from the group consisting of *Staphylococcus*, *Enterococcus*, *Streptococcus*, *Haemolyticus*, *Pseudomonas*, *Campylobacter*, *Enterobacter*, *Neisseria*, *Proteus*, *Salmonella*, *Simonsiella*, *Riemerella*, *Escherichia*, *Neisseria*, *Meningococcus*, *Moraxella*, *Kingella*, *Chromobacterium* and *Branhamella*.

59. **(Previously presented)** The method of claim 1, wherein the identification of the nucleotide sequences allows an identification of the polymorphism of an organism.

60. **(Previously presented)** The method of claim 1, wherein the identification of the nucleotide sequences allows the genotyping of an organism.

61. **(Previously presented)** The method of claim 1, wherein the identification of the nucleotide sequences allows the identification of a single nucleotide polymorphism.

62.-80. **Canceled**

81. **(Currently amended)** The method of claim 1, wherein said single-stranded capture nucleotide sequences comprise a nucleotide sequence of between about 15 and about 40 bases, which is able to specifically bind to said target nucleotide sequence without binding to said at least four homologous nucleotide sequences from other organisms.

82. **(Cancelled)**

83. **(Previously presented)** The method of claim 1, wherein the target nucleotide sequence presents a homology with other homologous nucleotide sequences higher than 30%.

84. **(Previously presented)** The method of claim 1, wherein other primers are present in the amplification step for the amplification of another nucleotide sequence.

85. **(Previously presented)** The method of claim 1, wherein the nucleotide sequence to be identified and/or quantified is an RNA sequence submitted to a reverse transcription of its 3' or 5' end by using a consensus primer.

86. **(Previously presented)** The method of claim 1, wherein the nucleotide sequences to be identified and/or quantified are from the *FemA* gene of Staphylococci species selected from the group consisting of *S. aureus*, *S. epidermidis*, *S. saprophyticus*, *S. hominis* and *S. haemolyticus*.

87. **(Previously presented)** The method of claim 1, wherein the solid support also bears another capture consensus nucleotide sequence able to bind to said target nucleotide sequence and to said at least four homologous nucleotide sequences.

88. **(Previously presented)** The method of claim 2, wherein the spacer is a non-specific nucleotide sequence of at least 20 nucleotides.

89. **(Currently amended)** The method of claim 1 ~~58~~, wherein the nucleotide sequences to be identified and/or quantified are from the ~~said gene is a~~ gene encoding sub-unit A of gyrase.

90. **(Previously presented)** The method of claim 54, wherein the Cytochrome P450 isoforms family comprises a Cytochrome P450 2D6 and a 2C19 isoforms.

91. **(Currently amended)** The method of claim 1, wherein the nucleotide sequences to be identified and/or quantified in the samples come from different animal species and genus belonging to families selected from the group consisting of: *Galinaceae*, *Leporidae*, *Suidae* and *Bovidae*.

92. **(Currently amended)** The method of claim 1, wherein the nucleotide sequences to be detected and/or quantified in the samples belong to specific fishes species selected from the group consisting of *G. morhua, G. macrocephalus, P. flesus, M. merluccius, O. mykiss, P. platessa, P. virens, S. salar, S. pilchardus, A. thazard, T. alalunga, T. obesus, R. hippoglossoides, S. trutta, S. sarda, T. thynnus, S. scombrus* belonging to genera selected from the group consisting of: ~~as~~ Auxis, Sarda, Scomber, Thunnus, Oncorhynch, Salmo, Merluccius, Pleuronectes, Platichtlys, Reinhardtius, Pollachius, Gadus, Sardina, from several families selected from the group consisting of: *Scombridae, Salmonidae, Merluccidae, Pleuronectidae, Gadidae* and *Clupeidae*.

93. **(Currently amended)** The method of claim 1, wherein the nucleotide sequences to be detected and/or quantified in the samples belong to different plant species and genus selected from the group consisting of ~~such as~~ Potato, tomato, oryza, zea, soja, wheat, barley, bean and carrot.

94. **(Currently amended)** The method of claim 1, wherein the nucleotide sequences to be detected and/or quantified in the samples are genetically modified organisms.